

Confining Safflower Pollen During Regeneration Of Germplasm Seed Stocks

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Abstract

The Western Regional Plant Introduction Station (WRPIS) maintains more than 2300 accessions of safflower (*Carthamus tinctorius* L.) for use as genetic resources. Periodic regeneration is needed to provide the quantity and quality of seed needed to keep this material available for distribution to researchers worldwide. To maintain the genetic purity of this material, outcrossing among accessions must be avoided during regeneration. Research has shown that natural outcrossing in safflower can range from zero to near 100%, but an average of 15 to 20% is most commonly reported. The degree of outcrossing depends on insect activity and variation in outcrossing potential of different genotypes. A large number of bee species forage on safflower blossoms, but honeybees are the most prominent pollinators. Wind pollination does not appear to be an important factor in safflower outcrossing. Crosses of wild, weedy *Carthamus* with safflower could result if plants were in close proximity. This would be most likely in species such as *C. oxyacantha*, *C. palaestinus*, and *C. flavescent* (= *persicus*). They are closely related and have the same chromosome number as safflower (n=12). However, these wild species appear to be extremely rare or non-existent in most safflower production areas in North America. At the WRPIS, screen cages fitting loosely around plants are constructed to exclude insect pollinators during seed regeneration. Genetically distinct, selfed seed is obtained for each accession; seed production is sufficient and germination is generally above 90%. This system would be impractical on a field scale, but there are large areas of North America where no safflower production currently occurs, and where no weedy safflower relatives are reported. Thus, isolation of transgenic safflower in suitable growing environments should be possible.